

us-09-978-188a-7.rsp

Sequence Alignment

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2004, 13:50:23 ; Search time 18 Seconds
(without alignments)
1423.251 Million cell updates/sec

Title: US-09-978-188A-7
Perfect score: 2527
Sequence: 1 MVKFPALTYWPLRFLVPL.....TMDPTEVTDIVEMRENE 492

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2527	100.0	492	1 ANKH HUMAN	Q9hcz1 homo sapien
2	2502	99.0	492	1 ANKH MOUSE	Q9jhz2 mus musculus
3	2489	98.5	492	1 ANKH RAT	P58366 rattus norv
4	2317	91.7	492	1 ANKH XENLA	P58367 xenopus lae
5	2158.5	85.4	501	1 ANKH BRARE	P58368 brachydanio
6	1528.5	60.5	355	1 ANKH TETNG	P58369 tetraodon n
7	114	4.5	416	1 LACY KLEBX	P18817 klebsiella
8	113.5	4.5	456	1 NUTM FODAN	P15578 podospira a
9	111	4.4	622	1 COX1 BACSU	P24010 bacillus su
10	109.5	4.3	610	1 PT2A ARATH	P46031 arabidopsis
11	107	4.2	422	1 EXUT BACSU	O34456 bacillus su
12	107	4.2	533	1 LAT2 RAT	Q9wvr6 rattus norv
13	106	4.2	401	1 YB77 METJA	O58578 methanococo
14	105	4.2	401	1 LSG1 HAEIN	P71399 haemophilus
15	105	4.2	676	1 HPI1 METAC	Q8tja9 methanosarc
16	103.5	4.1	398	1 BCR HAEIN	P45123 haemophilus
17	103	4.1	417	1 LACY ECOLI	P02920 escherichia
18	102.5	4.1	446	1 CITN SALTY	P31604 salmonella
19	102.5	4.1	531	1 LAT2 MOUSE	Q9qkw9 mus musculu
20	102.5	4.1	533	1 MVIN SHIR	O05467 rhizobium t
21	102.5	4.1	641	1 NUSM ALLMA	P50365 allomyces m
22	101.5	4.0	446	1 CITN SALDU	P31603 salmonella
23	100	4.0	982	1 YS96 CABEL	Q09965 caenorhabdi
24	99	3.9	385	1 Y421 METTH	O26521 methanobact
25	99	3.9	535	1 LAT2 HUMAN	Q9uh15 homo sapien
26	98.5	3.9	533	1 NUTM NEUCR	Q35140 neurospora
27	98.5	3.9	946	1 YBTC YEAST	P38250 saccharomyc
28	98	3.9	480	1 YE44 YEAST	P39981 saccharomyc
29	98	3.9	532	1 YAEW BACSU	P37555 bacillus su
30	97.5	3.9	346	1 FMLR PONPY	P79235 pongo pygma
31	97.5	3.9	3803	1 TRAI DROME	Q818u7 drosophila
32	97	3.8	402	1 YYCB BACSU	P37482 bacillus su
33	96.5	3.8	346	1 FMLR GORGO	P79176 gorilla gor

ALIGNMENTS

RESULT 1	ANKH HUMAN	ANKH HUMAN	STANDARD;	PRT;	492 AA.
ID	ANKH HUMAN	ANKH HUMAN	STANDARD;	PRT;	492 AA.
AC	Q9HCU1: Q9HCU2;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Progressive ankylosis protein homolog (ANK).				
GN	ANKH OR KIAA1581.				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20355194; PubMed=10894769;				
RA	Ho A.M., Johnson M.D., Kingsley D.M.;				
RT	"Role of the mouse ank gene in control of tissue calcification and arthritis";				
RL	Science 289:265-270(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=20450683; PubMed=1097877;				
RA	Nagase T., Kitano R., Nakayama M., Hiroawa M., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";				
RL	DNA Res. 7:273-281(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Ovary;				
RX	MEDLINE=22388257; PubMed=12477932;				
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldi M.P., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Wallaby S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,				
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,				
RA	Schneerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
RN	[4]				
RP	VARIANTS CMDJ SER-375 DEL; PHE-376 DEL AND ALA-380 INS.				
RX	MEDLINE=21313103; PubMed=11326338;				

P47234 citrobacter
Q8d9n8 vibrio vuln
P58164 escherichia
P24975 balaeopter
P11982 asterina pe
P45272 haemophilus
P35865 corynebacte
Q9w3v8 drosophila
P50367 rhizopus st
Q31y53 arabidopsis
Q00758 bacillus su
P03660 bacteriopho

RA Reichenberger E., Tiziani V., Watanabe S., Park L., Ueki Y.,
RA Santanna C., Baur S.T., Shiang R., Grange D.K., Beighon P.,
RA Gardner J., Hamersma H., Sellars S., Ramesar R., Lidral A.C.,
RA Sommer A., Raposo do Amaral C.M., Gorlin R.J., Mulliken J.B.,
RA Olsen B.R.,
RA "Autosomal dominant craniofacial dysplasia is caused by mutations
RT in the transmembrane protein ANK.",
RL Am. J. Hum. Genet. 68:1321-1326 (2001).
RN [5]
RN VARIANTS CMDJ ARG-292; ARG-331; SER-375 DEL; PHB-377 DEL; ALA-380 INS
RP AND ARG-389.
RX NUBLINE-21225282; PubMed:11326272;
RA Nuerberg P., Thiele H., Chandler D., Hoehne W., Cunningham M.L.,
RA Ritter H., Leschik G., Uhlmann K., Mischung C., Harrop K.,
RA Goldblatt J., Borochowitz Z.U., Kotzot D., Westermann F., Mundlos S.,
RA Braun H.-S., Laing N., Tinschert S.,
RA "Heterozygous mutations in ANKH, the human ortholog of the mouse
RT progressive ankylosis gene, result in craniofacial dysplasia.",
RL Nat. Genet. 28:37-41 (2001).
CC -1- FUNCTION: Regulates intra- and extracellular levels of inorganic
CC pyrophosphate (PPi), probably functioning as Ppi transporter.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Found in osteoblasts from mandibular bone and
CC from iliac bone; not detected in osteoclastic cells.
CC -1- DISEASE: Defects in ANKH are the cause of craniofacial
CC dysplasia Jackson type (CMDJ) [MIM:123000]. CMDJ is a rare
CC autosomal dominant skeletal disorder characterized by abnormal
CC bone formation and mineralization in membranous as well as
CC endochondral bones. Progressive thickening of the bones can cause
CC narrowing of cranial foramina and can lead to severe visual and
CC neurological impairment, such as facial palsy and deafness.
CC -1- SIMILARITY: BELONGS TO THE ANKH FAMILY.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL: AF274753; AAF88039.1; -
DR EMBL: AB046801; BAB13407.1; ALT_INIT.
DR EMBL: BC009835; AAH09835.1; -
DR EMBL: BC014526; AAH14526.1; -
DR GeneW; HGNC:15492; ANKH.
DR MIM; 605145; -
DR MIM; 123000; -
DR GO; GO:0016021; C: integral to membrane; IDA.
DR GO; GO:0019857; C: outer membrane; TAS.
DR GO; GO:0030504; P: inorganic diphosphate transporter activity; IDA.
DR GO; GO:0005315; P: locomotory behavior; NAS.
DR GO; GO:0007626; P: regulation of bone mineralization; TAS.
DR GO; GO:0030500; P: regulation of bone development; NAS.
DR GO; GO:0001501; P: skeletal development; NAS.
KW Transport; Phosphate transport; Transmembrane; Disease mutation;
KW Deafness.
FT DOMAIN 1 85 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 86 106 POTENTIAL.
FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 152 POTENTIAL.
FT DOMAIN 153 158 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT DOMAIN 180 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210 POTENTIAL.
FT DOMAIN 211 326 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 327 347 POTENTIAL.
FT DOMAIN 348 350 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 351 371 POTENTIAL.
FT DOMAIN 372 403 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 404 426 POTENTIAL.
FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 430 452 POTENTIAL.

FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
FT VARIANT 292 292 W -> R (in CMDJ).
FT 331 331 /FTID=VAR 012192.
FT 331 331 C -> R (in CMDJ).
FT 375 375 /FTID=VAR 012193.
FT 375 375 Missing (in CMDJ).
FT 376 376 /FTID=VAR 012194.
FT 376 376 Missing (in CMDJ).
FT 377 377 /FTID=VAR 012195.
FT 377 377 Missing (in CMDJ).
FT 380 380 /FTID=VAR 012196.
FT 389 389 /FTID=VAR 012197.
FT 389 389 G -> R (in CMDJ).
FT 78 78 /FTID=VAR 012198.
FT 78 78 N -> S (in REF. 1).
SQ SEQUENCE 492 AA; 54240 MW; 44BEE9089BDEC6B CRC64;
Query Match 100.0%; Score 2527; DB 1; Length 492;
Best Local Similarity 100.0%; Pred. No. 7.8e-195; Indels 0; Gaps 0;
Matches 492; Conservative 0; Mismatches 0;
QY 1 MKFPPALTYWPLRFLVPLGITNIAIDFGEQALNKGIAAVKEDAVEMLASGLAYSLMK 60
DB 1 MKFPPALTYWPLRFLVPLGITNIAIDFGEQALNKGIAAVKEDAVEMLASGLAYSLMK 60
QY 61 PFTGMSDFKNGVLGVFVNSKRDRTKAVLCMVVAGATAAAPHFTLIAYSDGLGYIINKLHV 120
DB 61 PFTGMSDFKNGVLGVFVNSKRDRTKAVLCMVVAGATAAAPHFTLIAYSDGLGYIINKLHV 120
QY 121 DESVGSKTRAFLYLAAPFPMDAMANTHAGILLKHKYSFLVGCASISDVIAQVFFVAILL 180
DB 121 DESVGSKTRAFLYLAAPFPMDAMANTHAGILLKHKYSFLVGCASISDVIAQVFFVAILL 180
QY 181 HSHLECEPILPILSYMGALVRCCTTCLGYGNKHNDIIPDRSGPBGDARIMKLSF 240
DB 181 HSHLECEPILPILSYMGALVRCCTTCLGYGNKHNDIIPDRSGPBGDARIMKLSF 240
QY 241 WPLALILATORISRPVNLVFSRDLGSSAAEAVALTATVPVGHMPYGLTEIRAVY 300
DB 241 WPLALILATORISRPVNLVFSRDLGSSAAEAVALTATVPVGHMPYGLTEIRAVY 300
QY 301 PAFDKNPNKLVSTNTVTAHHKKTFTVCMALSLTLCFVCMALSLTLCFVCMALSLTLCFV 360
DB 301 PAFDKNPNKLVSTNTVTAHHKKTFTVCMALSLTLCFVCMALSLTLCFVCMALSLTLCFV 360
QY 361 PAFELCVPLRIEFPVPTVVAHKTGMLTKTFLAPSVLRRIIVLASLVLPY 420
DB 361 PAFELCVPLRIEFPVPTVVAHKTGMLTKTFLAPSVLRRIIVLASLVLPY 420
QY 421 LGVHGATLGVSLLAGFVGGESTMVAIAACVYRKQKKKKMENESGATEDSAMTMPTEE 480
DB 421 LGVHGATLGVSLLAGFVGGESTMVAIAACVYRKQKKKKMENESGATEDSAMTMPTEE 480
QY 481 VTDIVEMKEENE 492
DB 481 VTDIVEMKEENE 492
RESULT 2
ANKH_MOUSE
ID ANKH_MOUSE STANDARD; PRT; 492 AA.
AC Q9JH22; O35138; O35139;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progressive ankylosis protein (Fn54 protein).
GN ANKH OR ANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

Db	2401	GGCTTGGCTTTTCCCTCGCCTTTCTCTGAGGTGCGATTAGAGCGAGTGCACATGAGCATCC	2460
Qy	2461	TTACTTTTGCATTTTAGTCTTTTACAGTGAACCTGAAGCTTTAAAGTCTCATCAGCATTTCTAA	2520
Db	2461	TTACTTTTGCATTTTAGTCTTTTACAGTGAACCTGAAGCTTTAAAGTCTCATCAGCATTTCTAA	2520
Qy	2521	TGCGAGGTTGCTCTAGGGTAACTTTTGAAGTACAGTATATTTACCTGGTCTGCTATCCTTA	2580
Db	2521	TGCGAGGTTGCTCTAGGGTAACTTTTGAAGTACAGTATATTTACCTGGTCTGCTATCCTTA	2580
Qy	2581	GTCAATAACTCTCGGGTACAGGTAATTTGAGAAATGTACTACGGTACTTCCCTCCACACCAT	2640
Db	2581	GTCAATAACTCTCGGGTACAGGTAATTTGAGAAATGTACTACGGTACTTCCCTCCACACCAT	2640
Qy	2641	ACGATAAAGCAAGACATTTTATACAGTACACAGAGTCACATATGTGGTCTCCCTGAAATA	2700
Db	2641	ACGATAAAGCAAGACATTTTATACAGTACACAGAGTCACATATGTGGTCTCCCTGAAATA	2700
Qy	2701	ACGCATTCGAAATCCCATGCGAGTGCAGTATATTTTCTTAAGTTTGGAAAGCAGGTTTTT	2760
Db	2701	ACGCATTCGAAATCCCATGCGAGTGCAGTATATTTTCTTAAGTTTGGAAAGCAGGTTTTT	2760
Qy	2761	CCCTTAAAAAATTTATAGACACGGTTCACATAATTTAGTACAGAAATTCCTAGACTGA	2820
Db	2761	CCCTTAAAAAATTTATAGACACGGTTCACATAATTTAGTACAGAAATTCCTAGACTGA	2820
Qy	2821	AAGAACCTAAACAAAAAATTTTAAAGATATATAATATATGCTGTATATGTTATGTAAT	2880
Db	2821	AAGAACCTAAACAAAAAATTTTAAAGATATATAATATATGCTGTATATGTTATGTAAT	2880
Qy	2881	TTATTTTAGCTATAPATACATTTCTCTATTTTCGATTTTCAATAAATGCTCTAATACA	2940
Db	2881	TTATTTTAGCTATAPATACATTTCTCTATTTTCGATTTTCAATAAATGCTCTAATACA	2940
Qy	2941	AAAAA 2945	
Db	2941	AAAAA 2945	
RESULT 3			
AB046801			
LOCUS	AB046801	3928 bp	mRNA linear PRI 22-FEB-2001
DEFINITION	Homo sapiens mRNA for KIAA1581 protein, partial cds.		
ACCESSION	AB046801		
VERSION	AB046801.1	GI:10047236	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (sites)		
TITLE	Nagase, T., Kikuno, R., Nakayama, M., Hirose, M. and Ohara, O.		
JOURNAL	Prediction of the coding sequences of unidentified human genes. XVIII. The complete sequences of 100 new cDNA clones from brain		
MEDLINE	DNA Res. 7 (4), 273-281 (2000)		
PUBMED	20450683		
REFERENCE	2 (bases 1 to 3928)		
AUTHORS	Ohara, O., Nagase, T. and Kikuno, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research, 1532-3, Yana, Kisarazu, Chiba		
FEATURES	282-0812, Japan (E-mail: cdna@fookazusa.or.jp, URL: http://www.kazusa.or.jp/huge, Tel: 81-438-52-3913, Fax: 81-438-52-3914)		
source	Location/Qualifiers		
	1. 3928		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="fj05690"		
	/note="vector:pBluescriptII SK plus"		

2960 TTATTTAGCTATAATACATTTCTCTATTTTCCTGATTTTCAATAAATAAATCTCTCTAATACA 3019

2941 AAA 2943

3020 ATA 3022

BC014526 3013 bp mRNA linear PRI 06-OCT-2003

Homo sapiens ankylosis, progressive homolog (mouse), mRNA (cDNA

clone MGC:11142 IMAGE:3837372), complete cds.

BC014526

BC014526.2 GI:33878622

MGC.

Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Altshuler,S.F., Zeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Schencz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

McKernan,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahy,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,

Schneerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2338257

12477932

2 (bases 1 to 3013)

Strausberg,R.

Direct Submission

Submitted (24-SEP-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

On Aug 19, 2003 this sequence version replaced gi:15778895.

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbio.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 14 Row: 9 Column: 4

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 21536393.

Location/Qualifiers

1. 3013

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

gene

CDS

Query Match 98.4%; Score 2896.8; DB 9; Length 3013;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2912; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

QY 27 CCGCAGAGTCCCTCGCGGAGCAGAGATGTGTGGGTGAGCCACCGCGGGGACTATGG 86

Db 1 CCGCAGAGTCCCTCGCGGAGCAGAGATGTGTGGGTGAGCCACCGCGGGGACTATGG 60

QY 87 TGAATTCCTCGCGGCTCAGCAGTCTGCGGCTGATCCGGTCTTCTGTCGCCCTCGGCA 146

Db 61 TGAATTCCTCGCGGCTCAGCAGTCTGCGGCTGATCCGGTCTTCTGTCGCCCTCGGCA 120

QY 147 TCACCAACATAGCAGTCTCGGGGAGCAGGCTTTGAACCGGGGATGCTGCTCTCA 206

Db 121 TCACCAACATAGCAGTCTCGGGGAGCAGGCTTTGAACCGGGGATGCTGCTCTCA 180

QY 207 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 266

Db 181 AGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

QY 267 TCACGGGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 326

Db 241 TCACGGGTCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300

QY 327 ACAGACCAAGGCGTCTGT 386

Db 301 ACAGACCAAGGCGTCTGT 360

QY 387 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 446

Db 361 CACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420

QY 447 AGTCGGTGGGAGCAGAGAGGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 506

Db 421 AGTCGGTGGGAGCAGAGAGGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480

QY 507 AGCGATGGCATGGACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566

Db 481 AGCGATGGCATGGACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540

QY 567 GATGTGCTCAATCTCAGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 626

Db 541 GATGTGCTCAATCTCAGATGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 600

QY 627 GTCACTGGAATGCCGGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 686

ORIGIN

Translation: MKFKALHYWELIRPLVPLGITNIAIDPGEALNRGIAAVKED

AVMLASYGLAYSLMKFFFTGPMSEDFKNGVLVFNKDRDKAVLCMVVAGAIATVHT

LIAYSOLGYIINKLHVDESVGSTRAPFLYLAFFDMAMTATGILLKHKY9FL

VGCASIDVIAQVFAVILHSHLECPILLIPLSLYMGALVCTTCLGYYKNTBAY

IIPDRSGELGGDVTIRKMLSVFVPAIDKNNPSKLVSTNTVAARIKKTFVCMAL

AILTATVPVCHMPYGLTEIRAVYPAIDKNNPSKLVSTNTVAARIKKTFVCMAL

SLILCFVMTFNVSEKILIDIGVDPAFELCVPLRIFSPRPVTVRAHLTGMLM

TLKXTFVLAPSSVLRIRIIVLASLVLPYLGHGATLGVSLLAGFVGESFWVAACY

VIKQKXKMNESATSEDSATMDMPPTBEVTDIVENRENE"